REMARKS

Claims 1-5, 9-14, and 128 are currently pending to which the Examiner provides several rejections that are listed here in the order in which they are addressed.

I. Claims 1-5, 9-14 and 128 are rejected under 35 USC ¶ 112 § 1 as the specification allegedly fails to comply with the written description requirement.

II. The Sequence Listing is allegedly not compliant.

The Examiner is requested to note the Applicants have provided related new Claims 138 and 139 for examination. Claim 139 lacks the "peptide effector" language.

I. The Claims Are Adequately Described By The Specification

A. SEQ ID NO: 67 Is Not New Matter

The Examiner states that:

> Applicant's insertion of SEQ ID NO:67 into the claims does not find support in the specification as originally filed since the sequence defined in the Sequence listing filed 1-29-07 does not find support in the specification as originally filed.

Office Action pg 3-4. The Applicants disagree because SEQ ID NO:67 was intended to reflect the nucleotide sequence amended into Claims 1 and 128 in Applicant's response mailed November 1, 2005. It is noted that the Examiner's subsequent Office Action January 19, 2006 erroneously reflected this amended sequence by creating a typographical error resulting in a - gtg - instead of a - gug - in positions 84-86. It appears that the Applicants unintentionally reproduced this typographical error in the Sequence Listing. The claims, however, have consistently maintained the – gug – portion since the November 1, 2005 amendment.

Nonetheless, without acquiescing to the Examiner's argument but to further the prosecution, the Applicants' business interests, and expedite the prosecution of this

application the Applicants' provide a corrected Supplemental Sequence Listing that corrects the above unintentional typographical error in SEQ ID NO: 67.[1]

The Applicants respectfully request that the Examiner withdraw the present rejection.

B. There Is Sufficient Description

The Examiner argues that the claims fail to comply with the written description requirement because "the specification as filed nor the claims provides sufficient description of the amino acid sequence of the entire genus of peptide effectors . . ." (office Action, page 4). Applicants cannot agree.

First and foremost, Claim 1 is directed to a *polynucleotide* and provides the *sequence*; Claim 1 does not claim the peptide effector. The Examiner is asked to take note that Claim 1 merely requires that the polynucleotide "is regulated by the interaction of the peptide effector." Similarly, Claim 128 is directed to a vector – not the peptide effector – and contains the same "is regulated" language. Indeed, Claim 1 can be re-written to exclude mention of the peptide effector (see new Claim 139).

Second, even if the claims were directed to a complex of polynucleotide and bound peptide effector – which they are not – this would be no different than claiming an antibody bound to a defined antigen. The Examiner is requested to consider that antibodies are routinely claimed – and yet no structural information concerning the antibody is typically provided or required where the antigen is well-defined. *See Synopsis of Application of Written Description Guidelines* at page 60, available at uspto.gov. It is understood in the art that binding partners – whether peptides or antibodies – can be generated by screening and that this screening does not require structural knowledge, let alone a "correlation" of structure with function.

Third, the law of written description has evolved considerably with the recent Federal Circuit decisions of *Capon v. Eshhar v. Dudas*, 418 F.3d 1349 (Fed. Cir. 2005) and *Falkner v. Inglis*, 79 USPQ2d 1001 (Fed. Cir. 2006). In the *Capon* case, the parties sought to patent a chimeric gene made of a first segment of DNA encoding the single-

[1] As originally stated in Applicants' response dated November 1,2005, specification support for this sequence is found in Figure 17b. Consequently, the sequence is not new matter.

chain variable region of an antibody, and a second segment of DNA encoding an endogenous protein. And yet, the specification (let alone the claim) did not contain a single sequence. The Board insisted the specification must provide the "structure, formula, chemical name, or physical properties" of such a DNA combination. The Federal Circuit reversed, noting that "the law must take cognizance of the scientific facts" which indicate that "the nucleotide sequences of the component DNA are known." Similarly, in the *Falkner* case, the party sought to patent a poxvirus vaccine lacking essential genes. However, the specification provided no sequences. Both the Board and the Federal Circuit found that the claims were nonetheless adequately supported. The Federal Circuit's decision was unanimous and contained the following warning:

> "Specifically, we hold, in accordance with our prior case law, that (1) examples are not necessary to support the adequacy of a written description (2) the written description standard may be met (as it is here) even where actual reduction to practice of an invention is absent; and (3) there is no *per se* rule that an adequate written description of an invention that involves a biological macromolecule must contain a recitation of known structure."

It is respectfully submitted that the present case is in an even better posture than the *Capon* or *Falkner* case. In the present case, the specification contains numerous sequences. Moreover, each independent claim contains the polynucleotide sequence. Furthermore, the specification contains working examples. Indeed, the Examiner is asked to take particular note of the following paragraph (emphasis added) in the specification which scientifically justifies the full scope of "peptide effectors":

> [0207] While the extent of Cyt18 activation of the aptazyme ligase was impressive, Cyt18 had previously been shown to similarly activate a group I self-splicing intron. In order to determine whether the ability to select for protein-dependent activation of ribozyme catalysis was specific to certain types of proteins *or was more general phenomena*, ribozyme ligases that could be activated by a protein not normally known to bind RNA, hen egg white lysozyme were isolated. Using the same selection scheme and progressive increases in stringency (FIG. 18C), regulatable, catalytically active nucleic acids that were activated by lysozyme were isolated in 11 cycles of selection and amplification. The final, selected population was activated about 800-fold by lysozyme (FIG. 18D) and an isolated clone, lys11-2, exhibited a 3100-fold activation, ligating with an observed rate of 0.6 h^{-1} in the presence of lysozyme but only 0.0002 h^{-1} without lysozyme.

Thus, a peptide not normally known to bind RNA, hen egg white lysozyme, was shown to work – illustrating that the results are NOT limited to certain types of proteins. Rather, the results are of a more general type, where ANY protein can be used.[2] Thus, it is not a question of the specification identifying just "two structures." The fact that hen egg white lysozyme could work illustrates the more "general phenomena." Furthermore, the Examiner has overlooked a number of other exemplified peptides:

> [0072] A protein-dependent, regulatable, catalytically active nucleic acid was also created and selected with an activity that was increased by 3,500-fold in the presence of its cognate protein effector, hen egg white lysozyme ... [and] ... turkey egg white lysozyme.

and,

> [0233] Rev-dependent RNA ligase ribozymes. An L1-N50 pool (10^{15} starting species) was subjected to an iterative regime of negative and positive selections for ligation activity. The pool was initially incubated with a biotinylated substrate and reactive species were removed; the pool was then mixed with the effector molecule, a 17 amino acid fragment of the HIV Rev protein, and reactive species were removed and amplified. The Rev peptide is a highly basic arginine rich motif whose natural function is as an RNA binding domain.

and,

> [0237] ... the Rev-dependent ligase was incubated with ... HIV Tat .... Activation was observed ... with HIV Tat peptide at about 30%. In addition, the complete Rev protein was able to activate the ligase about 10% as well as the peptide.

Applicants' Specification, USPAP 2003/0104520 @ indicated paragraphs [emphasis added]. The Applicants have described at least five (5) specific and working examples of a "peptide effector". This is sufficient to meet the intent of 35 USC 112, paragraph 1.

For all of the above reasons, the Applicants respectfully request that the Examiner withdraw the present rejection.

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[2] This, of course, makes scientific sense. When one screens without any bias, and merely looks for binding or activity, one will find positives within the population as long as the screening examines a large enough population.

II. The Sequence Listing Is Compliant

The Examiner objects to the Sequence Listing provided on 1-29-07 because it "... does not include the sequence recited in the instant claims". *Office Action, pg. 2.* The Applicants disagree and refer to the above argument provided in the Written Description section. As the Applicant's have provided a corrected Supplemental Sequence Listing, the Applicants now consider the Examiner's objections to Claims 1 and 128 moot.

The Applicants respectfully request that the Examiner withdraw the present objections.

CONCLUSION

The Applicants believe that the arguments set forth above traverse the Examiner's rejections and, therefore, request that all grounds for rejection be withdrawn for the reasons set above. Should the Examiner believe that a telephone interview would aid in the prosecution of this application, the Applicants encourage the Examiner to call the undersigned collect at 617.984.0616.

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By: _____

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